1 INTERPRETIVE SUMMARY

2 Relative importance of herd-level risk factors for probability of infection with

3 paratuberculosis in Irish dairy herds

4 McAloon

- 5 The objective of this study was to identify the most important herd-level risk factors for
- 6 Johne's Disease in dairy herds. Analysis of management practices, animal movement and
- 7 diagnostic test data from 925 Irish dairy herds identified routine use of the calving area for
- 8 sick or lame cows, and length of time spent in the calving pen as the most important risk
- 9 factors in Irish dairy herds.

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13 RISK FACTORS FOR PARATUBERCULOSIS

- 14 Relative importance of herd-level risk factors for probability of infection with
- 15 paratuberculosis in Irish dairy herds
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23 ABSTRACT

Control of paratuberculosis is challenging due to the relatively poor performance of 24 25 diagnostic tests, a prolonged incubation period and protracted environmental survival. Prioritisation of herd-level interventions is not possible because putative risk factors are often 26 27 not supported by risk factor studies. The objective for this study was to investigate the 28 relative importance of risk factors for an increased probability of herd paratuberculosis 29 infection. Risk assessment data, comprehensive animal purchase history and diagnostic test data were available for 936 Irish dairy herds. Both logistic regression and a Bayesian beta 30 31 regression on the outcome of a Latent Class Analysis were conducted. Population Attributable Fractions and proportional reduction in variance explained were calculated for 32 each variable in the logistic and Bayesian models respectively. Routine use of the calving 33 area for sick or lame cows was found to be a significant explanatory covariate in both 34 models. Purchasing behaviour for the previous 10 years was not found to be significant. For 35 36 the logistic model, length of time calves spend in the calving pen (25%), and routine use of

the calving pen for sick or lame animals (14%) had the highest attributable fractions. For the
Bayesian model, the overall R-squared was 16%. Dry cow cleanliness (7%) and routine use
of the calving area for sick or lame cows (6%) and had the highest proportional reduction in
variance explained. These findings provide support for several management practices
commonly recommended as part of paratuberculosis control programmes, however a large
proportion of the observed variation in probability of infection remained unexplained
suggesting other important risks factors may exist.

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INTRODUCTION

Bovine paratuberculosis, also called Johne's Disease (**JD**) is characterised by chronic 45 granulomatous enteritis which manifests clinically as a protein-losing enteropathy causing 46 diarrhoea, hypoproteinaemia, emaciation and eventually death (Sweeney et al., 2012). 47 Adverse effects on animal productivity in terms of lower milk yield (McAloon et al., 2016), 48 higher cull rates (Hendrick et al., 2005), reduced value for culled animals (Richardson and 49 More, 2009), possible adverse effects on fertility (Johnson-Ifearulundu et al., 2000) and 50 losses due to continued spread of infection are key drivers in the attempt to control the 51 disease at farm level. In addition, some research exists to suggest that the aetiologic pathogen 52 53 Mycobacterium avium subspecies paratuberculosis (MAP) may pose a zoonotic risk 54 (Chiodini et al., 2012).

Control of JD is difficult due to the relatively poor performance of diagnostic tests (Nielsen and Toft, 2008), a prolonged incubation period (Sweeney et al., 2011) and protracted environmental survival (Whittington et al., 2004). Several simulation studies have concluded that test and cull programmes are unlikely to be effective in isolation and that control of the disease on farm should centre primarily on closing infection routes, ideally in combination with testing and culling (Kudahl et al., 2011; Lu et al., 2010; Robins et al., 2015). However, there is little empirical evidence to support many of the specific interventions introduced at 62 herd level to reduce the probability of introduction and transmission of disease. Although several risk factor studies have been conducted, results often fail to agree with putative risk 63 factors that inform key aspects of control programmes, making prioritisation of 64 implementable control measures difficult (McAloon et al., 2015). 65 At least part of the disparity in these studies may be due to misclassification of positive and 66 67 negative herds. Conventionally, herd level risk factor studies are conducted by attributing an infection status to each herd based on a set number of test reactors. However, such 68 dichotomised approaches may discard important information regarding the likelihood of 69 70 infection and may be biased in larger herds due to imperfect test specificity. The use of Bayesian Latent Class methods allows the estimation of a probability of infection 71 72 for each herd conditional on the test characteristics, number of test positive animals and the 73 total number of animals in the herd (Branscum et al., 2004). In addition, Bayesian methods account for uncertainty associated with model parameters by modelling each parameter as a 74 75 random variable with an associated probability distribution. Bayesian inference allows direct 76 inference on the parameter of interest, conditional on the observed data and the prior distributions (Messam et al., 2008). 77 In Ireland, control of non-statutory diseases such as JD is coordinated by Animal Health 78 Ireland (AHI) (More et al., 2011). In 2013, a pilot Voluntary Johne's Disease Control 79 80 Programme was introduced which combined annual testing of all animals over 24 months of age with an on-farm Risk Assessment and Management Plan (RAMP) that captured herd 81 management practices relevant to JD. RAMP has been widely adopted across many countries 82

83 with recognisable control programmes (Geraghty et al., 2014). The Risk Assessment (**RA**)

84 component involves assigning risk scores to different management procedures and areas

85 based on observations and farmer reported practice. In addition, within the Irish system,

86	animal movement data for the herd is provided for the practitioner to assess bioexclusion
87	risks. The outcome of the RA is used to inform a Management Plan (\mathbf{MP}) and, in national
88	programmes, may have some bearing on herd categorisation or herd risk score.
89	A reduction in animal-level test positivity associated with the implementation of management
90	practices has been found in a number of small scale investigations on demonstration or study
91	herds using the RAMP approach (Ferrouillet et al., 2009; Pillars et al., 2011; Espejo et al.,
92	2012) but progress has not been reproduced in larger studies on commercial farms (Sorge et
93	al., 2011). Furthermore, to the authors' knowledge there are no studies available investigating
94	the risk associated with RAMP scores in combination with comprehensive herd purchase
95	history, or modelling herd level infection status on a probabilistic scale.
96	The objective of this study was to identify and evaluate the relative importance of risk factors
97	for JD probability of infection using diagnostic test results, RA scores and animal movement
98	history for herds enrolled in the national voluntary Johne's Disease Control Programme.
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110 extracted for the period beginning 1st November 2013 and ending 30th December 2014 and included anonymised cow and herd identifiers, test-date, sample-to-positive (S/P) ratio, 111 laboratory interpretation (negative, suspect, positive), sample type (blood or milk), testing 112 laboratory (test kit) and county. Diagnostic test data were available for 1,040 herds. 113 Given that the time frame for extraction exceeded 12 months, several herds had results from 114 115 more than one herd screen. To reduce the potential for reverse causality, i.e. the effect of changes in management occurring as a result of a positive diagnosis, the last herd screen 116 occurring before the RAMP was preferentially selected, followed by the soonest herd screen 117 occurring after the RAMP. Test and animal movement data were extracted separately and 118 datasets were aligned using coded herd identifiers. An additional binary variable was created 119 to investigate the effect of having the test before (1) versus after (0) the RAMP. The values 120 for sensitivity (Se) and specificity (Sp) used in the models were appropriate for a single test. 121 In addition to ongoing testing, enrolled herds were required to have an annual RAMP carried 122 123 out by a programme approved veterinary practitioner. The RAMP contained questions on the history of the disease on each farm as well as the risk of introduction of infection from 124 sources other than animal movement -e.g. colostrum, slurry contractors etc. The 125 biocontainment component of the RAMP consisted of an additional 28 questions regarding 126 management practices and observations made on the farm at the day of the visit, which were 127 deemed to be relevant to the spread of JD. 128

In the RA used in the Irish programme, questions were scored using an ordinal scale of 1, 4, 7 and 10. Within the AHI programme, this method was used to reduce the potential for subjectivity that might be associated with the use of a continuous scale, since each specific management practice may be associated with a particular score on the ordinal scale. In addition, the use of 1, 4, 7 and 10 rather than 1, 2, 3 and 4 was used as a means of weighting the risk associated with each management practice. Higher scores were associated with
increased risk of transmission. However, for this study, RA scores were modelled as
categorical variables, thereby reflecting the risk associated with specific practices rather than
the risk scores *per se* and ensuring that the scale used would have no effect on the model
outcome. Questions asked as part of the RAMP are shown in Table 1.

139 To assist in assessing bioexclusion, the RAMP was pre-populated with animal movement data for the herd over the preceding 10 years. Movement data included herd size, number of 140 male and female introductions, number of source herds and number of overseas imports for 141 every year from 2005 to 2014. Herd sizes less than 20 in 2014 were dropped from the 142 analysis. Herd size was next summarised across the 10-year period: herds that had a herd size 143 of <105% of herd size in 2005 were categorised as non-growing herds; the remaining herds 144 were then broken into mild, moderate and large growth by categorising the percentage growth 145 into 3 equal quantiles: 5-25%, 26-46% and >46%. 146

147 Movement and herd size data were then aggregated over two 5-year periods, 2005-2009 and 2010-2014. Within each 5-year period, herds were described as "closed" if no purchases had 148 been made, herds where no females were purchased and males were purchased at <5% of the 149 overall herd size were described as "Replacement bulls only", for the remaining herds, the 150 number of female purchases was averaged across the 5-year period and broken into 3 equal 151 152 quantiles: low, medium and high replacement purchase. Given small number of herds were in the "closed" category for each 5-year period, this category was combined with "Replacement 153 bulls only" for the analysis. An additional binary variable was created to identify herds where 154 males were purchased at greater than 5% of the overall herd size. These herds were 155 considered likely to be purchasing male animals for beef production in addition to the dairy 156 enterprise. Finally, the number of source herds purchased from each year was averaged 157 across each 5-year period. 158

Herds were removed from the dataset when one or more of the 3 components of the scheme:
diagnostic test results, herd movement history and RAMP results, were missing or
incomplete. The final dataset included data from 925 herds.

162 Analytical Models

Model 1; Logistic regression analysis. The outcome variable was herd infection 163 164 status (positive or negative) and herds were defined as positive when they had 2 or more cows with positive tests. A cut point of 2 positive cows was used to account for imperfect test 165 specificity; with herd sizes represented in this study, it was less likely that two positive results 166 would both be false positives. In addition, for the purposes of comparison, the final model 167 was reassessed with a cut-point of 1 reactor, the final single reactor model is included as 168 supplementary material (Supplementary Material 1 - Table 1). Data analysis was conducted 169 170 in R-studio version 1.0.44 (The R Core Team, 2016). Individual explanatory covariates were initially investigated within a univariable logistic regression framework and carried forward 171 for multivariable regression analysis when P<0.2. Before addition to the multivariable model, 172 covariates were assessed for correlation. When 2 variables were highly correlated (>0.8), one 173 was selected and brought forward for multivariable analysis based on whichever variable 174 175 resulted in the model with the lowest Akaike Information Criterion (AIC). Variables dropped 176 due to collinearity were replaced into the final model to test for significance. The model was 177 constructed using a forward stepwise elimination and variables with a significance 178 probability P<0.05 were retained in the model. Herd size and test medium were forced into the model from the beginning of the multivariate analysis to account for the potential 179 confounding effect of these variables on test sensitivity and specificity. In addition, for the 180 181 purpose of comparison, the model was reconstructed using the AIC solely as the selection criteria. Finally, the Population Attributable Fraction (**PAF**) was calculated for each variable 182 in the model based on distribution of exposure in cases (Hanley, 2001); 183

184 PAF=
$$\frac{\text{RR-1}}{\text{RR}} \times \frac{\text{number of exposed cases}}{\text{overall number of cases}}$$

Adjusted relative risks were calculated from the Odds Ratios of the final model using themethod described by Zhang (1998).

Model 2; Bayesian analysis. This analysis was conducted in two stages. First, a
probability of infection for each herd was estimated using a Bayesian latent class model. This
model had the same structure, and was implemented using the same methods as described in
McAloon et al.(2016a). Briefly, the number of test positive animals in a given herd was
assumed to follow a binomial distribution with a probability equal to the apparent prevalence
and n equal to the number of animals tested. The apparent prevalence (AP) was related to the
true prevalence (TP) and the test sensitivity (Se), and specificity (Sp) by the formula;

194
$$AP = TP x Se + (1 - TP) x (1 - Sp)$$
 (2)

TP was modelled as a mixture of a Bernoulli distribution, with a probability equal to the probability of infection for the herd, and a beta distribution equal to the within herd true prevalence.

In the second step, the mean probability of infection for each herd was used as the outcome variable in a Bayesian beta regression model with a logit link (Branscum et al., 2007). The model was built using a forward stepwise analysis and variables were retained in the model when the 95% credible interval did not include zero.

 $203 \qquad \mu_i \sim beta(a_i, b_i) \tag{3}$

$$204 a_i = \psi_i \times \gamma (4)$$

$$205 \qquad b_i = (1 - \psi_i) \times \gamma \tag{5}$$

$$206 \quad \operatorname{logit}(\psi) <-\beta_0 + \beta_1 X_1 \dots \tag{6}$$

207
$$\gamma \sim \text{gamma}(G_1, G_2)$$
 (7)

208 where μ_i was the probability of infection for the i-th herd which was modelled by a beta 209 distribution. To facilitate incorporation of the covariate information into the regression 210 model, the beta distribution was parameterised in terms of its mean, ψ , and a parameter related to its variance, γ (Bransum et al., 2007). A logit link was used to estimate the 211 regression coefficient, β , for each covariate, X. G₁ and G₂ were the shape and scale 212 parameters for the gamma distribution, γ . Larger values of γ correspond to less heterogeneity 213 in the data. For this analysis, a prior gamma distribution with a low mean and high variance 214 was used (G₁=G₂=0.01). 215

Diffuse normal distributions (mean = 0, precision = 0.01) were used for the priors of each
coefficient in the model. Model outcomes for each covariate were reported as probability of
infection by converting the coefficients according to the formula;

219
$$p = \frac{1}{1 + e^{-(\beta_0 + \sum \beta_j X_j)}}$$
 (8)

Where *p* is the probability of infection, β_0 is the intercept and β_j is the coefficient of the j-th covariate, X_j (Dohoo et al., 2010). To fit the model, mean probabilities of infection less than 0.01 (n=8) were rounded to 0.01 and those greater than 0.99 (n=100) to 0.99.

Model fit was assessed using posterior predictive simulations (Gelman et al., 2000). The
predictive simulation incorporated within the model was;

225
$$\operatorname{Pred}_{\mu_i} \sim \operatorname{beta}(a_i, b_i)$$
 (9)

226 Predµi was monitored for the final 5000 iterations of the overall simulation. Predicted

227 probability of infection was compared to the probability of infection outcome from the latent

class model and the mean difference and the mean squared difference was used to compare

229	models. The proportional reduction in variance explained was calculated for each variable by
230	removing each variable in turn from the full model, re-estimating model parameters and,
231	calculating the difference in R-squared relative to the full model.
232	The model was implemented in WinBUGS 1.4.1 (Lunn et al., 2000), the first 5,000 iterations
233	were discarded as burn in, by which time convergence had occurred, and 15,000 iterations
234	used for posterior inference. Convergence was assessed by visual assessment of the chain as
235	well as by running multiple chains from dispersed starting values (Christensen et al., 2012).
236	The code for analysis is provided as supplementary material (Supplementary Material 2).
237	
238	RESULTS
239	Descriptive Statistics
240	925 herds were present in the final dataset. Overall median herd size was 80, Using a cut-
241	point of 2 reactors, 265 herds were positive, giving an apparent prevalence of 0.29. RAMP
242	scores are summarised in Figure 1 and animal purchase data for the 10 years prior to
243	diagnostic testing are summarised in Table 2.
244	Median herd growth from 2005 to 2015 was 25%. From 2005-2009 only 30 herds were
245	classified as closed, with a further 70 herds classified as replacement bull purchases only.
246	Similarly, from 2010-2014, 37 and 109 herds were closed or replacement bull only. From
247	2005-2009, 30% of herds purchased replacement females at an annual average of more than
248	7.5% of the total herds size, whilst from 2010-2014, the equivalent figure was 28%. In each
249	5-year block the mean annual number of source herds was more than 1 for 54% of the herds
250	in 2005-2009 and 38% in 2010-2014.

251 Model Outcomes

252

Model 1; Logistic regression.

The outputs from the final multivariable logistic regression model are shown in Table 3. The 253 reference category for each variable has been selected to avoid negative coefficients. Herd 254 255 size was positively associated with herd positivity with an odds ratio of 1.01 for each additional animal. Herds testing with milk were 1.57 times as likely to test positive as those 256 testing with blood. A large seasonal effect was apparent with herds testing in January 2.1 257 258 times as likely to test positive as those tested in May. Herds where pooled colostrum was used for more than 10% of the calves were 2.1 times as likely to be positive compared to 259 those herds where calves were fed colostrum from their own test-negative dam, this category 260 had a PAF of 11.6%. Herds where weaned heifers were grazed near adult animals, but 261 without direct or indirect contact were 1.7 times as likely to test positive, and had a PAF of 262 263 10.5%, as those where direct or indirect contact was possible. Herds where the milking cow 264 environment had clearly visible manure contamination were 1.7 times as likely to be defined as positive compared to herds where only trace amounts of manure were visible with a PAF 265 of 7.6%. Herds where the calving area was routinely used for housing sick and lame cows 266 were 2.2 times as likely to be positive than those where the calving area was never used for 267 non-calving cows and had a PAF of 14.2%. Herds where more than 50% of the calves were 268 removed from the dam within 30 minutes of birth were 2.3 times as likely to test positive as 269 270 those where 90% of the calves were removed within 15 minutes of birth, the PAF of this 271 variable was 24.7%. Finally, herds that experienced small growth (5-25%) were 1.7 times as likely to test positive as those that expanded to a high (>50%) growth in herd size. 272

273 *Model 2; Bayesian Model.* Outputs from the final Bayesian beta-regression model are
274 shown in Table 4. Overall the model explained 16% of the variation, indicating that a
275 considerable amount of the variation in the probability of a herd being positive remained

276 unexplained. The reported presence of previous clinical or test positive animals was responsible for 22.6% of the overall variance explained (R-squared) and resulted in a mean 277 probability of infection (95% probability interval) of 0.72 (0.66-0.77). A strong seasonal 278 279 effect was again observed which was responsible for 35% of the overall R-squared, with herds testing in January having a probability of infection of 0.77 (0.69, 0.83). The proportion 280 of the herd tested comprised 3.2% of the overall R-squared and was negatively associated 281 with the probability of infection. The probability of infection dropped by 5% with each 282 additional 10% of the herd tested. Feeding of forages to weaned heifers that had been spread 283 284 with slurry in the previous season increased the probability of infection by 8% (0-16%). Dry cow cleanliness comprised 7.1% of the overall R-squared and herds where dry cows had no 285 faecal contamination visible had a mean probability of infection of 0.67, compared to 0.60 in 286 287 herds where faecal contamination was visible on the legs but not extending above the dewclaws. The use of the calving pen for non-calving animals comprised 5.8% of the overall 288 R-squared and herds where the calving pen was routinely used for sick or lame animals had a 289 290 probability of infection of 0.69 (0.65-0.74).

291

DISCUSSION

The present study used a combination of frequentist and Bayesian methods to investigate risk factors for positivity and infection probability in Irish dairy herds using data collected as part of the AHI voluntary programme.

In the logistic regression model, the speed with which calves were removed from the calving pen was the most important variable (PAF = 24.7%). Herds in which >90% calves were removed within 15 minutes of birth had the lowest risk of being positive, with herds where calves were still removed within 30 minutes were 2.2 times as likely to be positive. In this case the large PAF is caused by a combination of the relatively large odds ratio, combined 300 with the large proportion of herds within the higher risk category (n=507). The practice of removing the calf immediately from the dam is commonly advocated for the purpose of 301 paratuberculosis control however, despite investigating this risk factor, a number of studies 302 303 have failed to find this practice associated with an increased risk of positivity (Johnson-Ifearulundu and Kaneene, 1998; Wells and Wagnher, 2000; Nielsen and Toft. 2011). 304 However, Cashman et al. (2008), found an increased risk of culturing MAP from milk filters 305 306 in herds where a greater proportion of calvings where not supervised. Interestingly, the practice of immediate separation from the dam is also recommended for the control of calf 307 308 diseases (McGuirk and Collins, 2004), although studies into the benefit of calf removal have been equivocal (Weary and Chua, 2000; Trotz-Williams et al., 2007), McAloon et al., 2016b 309 recently found improved passive transfer in calves removed immediately from the calving 310 311 pen, compared with those spending more than 30minutes with the dam.

The use of the calving pen to house sick or lame animals was the second most important 312 management factor in both the Bayesian and logistic model with a proportional reduction in 313 R-squared of 5.8% and a PAF of 14.2%). Herds that routinely used the calving pen for sick or 314 lame cows had a mean probability of infection of 0.69 (0.65-0.74) and were 2.3 times as 315 316 likely to be defined as positive compared with herds in which the calving pen was never used for sick or lame cows. The use of the calving pen for sick or lame cows is often discouraged 317 318 as part of JD control programmes (Sweeney et al., 2012). This is based on the rationale that 319 cows that are subclinically infected with JD are more likely to be susceptible and therefore affected with other diseases but there appears to be little empirical evidence to support this 320 claim. It is however likely that "sick" cows would also include those suffering from 321 322 symptoms of clinical JD and this practice could facilitate disease transmission. In addition, 323 routine use of the calving pen for sick animals could be an indicator of increased stocking

density and insufficient building space, potentially resulting in increased exposure of calvesto infected faecal material.

The source of colostrum was significant in the logistic regression model and had a PAF 326 11.6%). However, this variable was not significant in the Bayesian model. Herds in which 327 over 10% of calves were fed colostrum from sources other than the dam (Risk Score 10) were 328 329 2.1 times as likely to be defined positive compared with herds in which dam-only colostrum was practiced. Nielsen et al. (2008) found that calves fed colostrum from multiple sources 330 were 1.2 times as likely to be positive than those fed dam-only colostrum. However, this 331 finding is not consistent. For example, in a longitudinal study, Pithua et al. (2011) found that 332 calves fed PCR-positive colostrum were not at a significantly greater risk of testing positive 333 as adults compared to those fed PCR-negative colostrum. In contrast, the same author found 334 335 that calves fed a commercial colostrum replacer were less likely to be identified as positive as adults than those fed conventional colostrum (Pithua et al., 2009). Similarly, Stabel (2008) 336 found that colostrum pasteurisation reduced the incidence of disease in calves as measured by 337 interferon gamma. However, in the long-term, risk of infection for this cohort of calves was 338 not different between groups (Godden et al., 2015). 339

Dry cow cleanliness was significantly associated with probability of infection in the Bayesian 340 model and was responsible for a reduction in R-squared of 7.1%). The finding that the lowest 341 dry cow contamination score was associated with an increased risk of infection compared to 342 the second lowest score seems counterintuitive. This finding could potentially be explained 343 given the seasonal calving system operated on Irish dairy herds, i.e. the fact that the dry cow 344 pen is not in use for a large majority of the year. However, whenever the month when the 345 RAMP was conducted was forced into the model, the variable remained significant 346 suggesting that the time when the RAMP was conducted was not confounding this variable. 347

348 It is worth noting that risk scores of 7 and 10 were associated with increased risk compared to 349 risk score 4 although these associations were not significant.

Similarly, the finding that herds where heifers were housed or grazed near cows but had no 350 direct contact (Q23) were at greater risk of testing positive compared with those where there 351 was direct contact or heifers were exposed via run-off or slurry spreading, is difficult to 352 353 explain. The susceptibility to infection has been shown to decrease with age (Windsor and Whittington, 2010), however, more recently, Mortier et al. (2013) demonstrated that calves 354 up to the age of 12 months could be infected with both high and low doses of MAP. Despite 355 been identified as the lowest risk category for this model, the large proportion of herds where 356 weaned heifers had direct or indirect contact with adult cows (45%) is a significant concern. 357 The milking cow environment score had a PAF of 7.6% with herds where manure was clearly 358 359 visible were 1.7 times as likely to test positive as those where trace amounts of manure was visible. Although infection of adult animals is possible with sufficiently high doses of MAP 360 361 (Whittington and Windsor, 2010), in this case it is more likely that the finding is indicative of the overall hygiene of the farm, rather than the specific risk to adult animals per se. 362 363 In the Bayesian model, the feeding of forages that had received slurry from adult animals was significantly associated with the probability of infection, however this variable only 364 comprised 1.3% of the overall variation. Interestingly, a similar finding was observed in a 365 North American study (Obasanjo et al., 1997). In contrast, Kohl et al. (2010) was unable to 366 culture MAP from baled grass silage following inoculation, although samples were positive 367 by PCR. The authors in that study suggested that conserved forages constituted a minor risk 368 369 for transmission. In a pasture based system where conserved forages are consumed during the housed period, avoiding the use of slurry on harvested grass may difficult to avoid, which is 370 reflected in the high proportion of herds in the higher risk category (95%). In addition, on 371

many farms, avoiding spreading slurry on grass harvested for younger animals would
necessitate segregation of conserved forage for different age groups of animals. Furthermore,
increased application on adult ground would lead to an increase in potassium content (Soder
and Stout, 2003), resulting in an increased Dietary Cation Anion Difference and therefore an
increased risk of hypocalcaemia (Goff, 2004).

377 The change in herd size from 2005 to 2014 was only significant in the logistic model with a PAF of 6.7%. In that case, the lowest risk of testing positive was observed in herds that had 378 undergone significant expansion (>50%) over the 10-year period. Anecdotally, herd 379 380 expansion has been associated with an increased risk of poor heath in general. However, in a previous Irish study, Jago and Berry (2011) found improved reproductive performance in 381 dairy herds undergoing higher levels of expansion suggesting that this finding could be 382 383 confounded by improved management in general on these farms. In addition, the same study found that the average parity number decreased in herds as the rate of expansion increased. 384 The sensitivity of the ELISA is known to increase with increased age (Nielsen et al., 2013), 385 therefore as the mean age of the herd decreases, the effective herd level sensitivity of the 386 ELISA screen is also likely to have decreased. 387

In the Bayesian model, previous presence of test positive or clinical cases of JD explained the largest proportion of variance explained (41%), however, in the logistic model, this variable had a PAF of 12.6%. The finding is unsurprising and highlights awareness of the herd infection status in many herds. It was decided to couple this variable with whether or not the RAMP had been conducted prior to or after the herd screen in an attempt to remove any possible confounding associated with prior knowledge of the disease in the herd. When the variable was removed from the model, all of the variables remained significant. 395 Given the imperfect specificity of the test, herd size was included as a variable, largely to account for confounding since larger herds would have an inherently greater risk of having 396 false positive test results. In agreement with this, herd size was found to be significant in the 397 398 logistic model, whereas in the Bayesian model, herd size was not significant. However, previous studies have documented increased risk of infection status in association with 399 increased herd size. Collins (1994) found that larger herds in Wisconsin were more likely to 400 401 be defined positive based on serological methods, however this association was not statistically significant. Similarly, Daniels et al., (2002) found that clinical disease was more 402 403 likely to be present on Scottish farms in the preceding 10 years when herd size was larger. Finally, based on analysis of submitted laboratory samples, Barrett et al. (2011), found a 404 405 significant association between herd positivity and herd size.

406 To the authors' knowledge this study represents the first use of herd level outputs from a Bayesian latent class model to fit a beta regression on herd level risk factors. Furthermore, 407 the use of PAF from a classical logistic regression model has not yet been used to investigate 408 the relative importance of risk factors for paratuberculosis. The Bayesian model reduced the 409 risk for misclassification due to imperfect test performance as test Se and Sp were 410 411 incorporated within the latent class model. On the other hand, the logistic model was based 412 on the binary outcome of assigned herd status facilitated the use of PAF, giving a more 413 intuitive impression of the relative importance of significant risk factors. Both methods are 414 limited by the sampling method in this study. The Irish JD control programme is voluntary and therefore may not be representative of the average Irish dairy farm. In addition, the study 415 416 utilised a cross sectional design based on a single test, single RA strategy. Although the 417 recommendation from the national programme is to conduct the RA prior to testing, it is possible that testing may have been conducted prior to the completion of the RA, prompting 418 the introduction of management changes and thereby introducing the risk of reverse causality 419

into the analysis. The authors attempted to reduce this risk by using RA data from the first
year of the programme. Given that the management practices identified as significant in this
are biologically plausible and largely agree with putative risk factors, it seems unlikely that
reverse causality was a significant issue in this analysis.

An unforeseen, outcome of the analysis was the strong seasonal effect that was observed in 424 425 both models. In each model, January, February and March were associated with a greater risk of positivity. The risk decreased in April, May and June before increasing again in the 426 autumn and winter. Within the Irish system, seasonality has the potential to be confounded by 427 428 stage of lactation and therefore milk yield. Nielsen and Toft (2012), found that the risk of being test positive on milk ELISA was greatly increased in the first 7 DIM and increased 429 linearly over the course of the lactation after correcting for milk yield which appeared to have 430 431 a diluting effect. To investigate the current dataset further, we separated the dataset into herds using milk and those using blood. Although the lowest risk month for both datasets was the 432 same, i.e. May, different temporal trends were apparent depending on the test media used. In 433 the milk dataset, the risk steadily increased from March to August with a large peak in 434 September before declining again from September to December. With the serum dataset, the 435 436 highest risk of test positivity was in January with a decline until May, with a second smaller peak in July. These findings require further investigation to examine whether this trend 437 438 repeats in subsequent years.

439

CONCLUSIONS

This study demonstrates the use of PAF and Bayesian beta-regression as a means of
investigating the relative importance of herd-level interventions on a national scale for the
control of paratuberculosis. The findings of this study suggest that the national control
programme should emphasise avoiding the use of the calving pen to house sick and/or lame

444	cows, reducing the length of time calves spend in the calving pen to less than 15 minutes and
445	reducing the prevalence of pooled colostrum feeding as key interventions to reduce the
446	prevalence of paratuberculosis in Irish dairy herds. It should also be noted however, that a
447	large proportion of the observed variation in probability of infection remained unexplained
448	suggesting other important risks factors may exist.
449	AKNOWLEDGEMENTS
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560

- 561 Table 1. Questions asked as part of on-farm Risk Assessment (RA) conducted on 925 dairy
- 562 herds enrolled in the Irish national Johne's Disease Control Programme
 - Q1. Have you ever completed a Johne's Disease herd test?
 - Q2. Has there been any suspect cases of JD on the farm?
 - Q3. Have you had any confirmed clinical JD or test positive cows in your herd?
 - Q4. Do you use your own equipment to spread slurry on your farm?
 - Q5. Do you spread cattle/slurry from other herds on your pasture?
 - Q6. Do you graze cattle purchased by you for fattening on your pasture?
 - Q7. Do you graze cattle/cows on commonage or with cattle from other herds
 - Q8. Do you graze on rented ground?
 - Q9. Do you use contract rearers or rear calves/heifers under a different herd number?
 - Q10. Do sheep cograze on this farm?
 - Q11. Are calves fed colostrum from own mother or from known low risk colostrum cows or artificial
 - Q12. Are at least 3 litres of colostrum (first milking) consumed within the first 2 hours?
 - Q13. Are calves fed on low risk whole milk
 - Q14. How often is non-saleable whole milk (high risk) fed?
 - Q15. Are calves housed in individual or group pens in the first week?
 - Q16. Is there exposure to cow manure in the calf housing or grazing area?
 - Q17. Is there exposure to cow manure by watering or feeding utensils?
 - Q18. Are calves fed forages that have received slurry from adult animals within the last year?
 - Q19. Do you feed or have you fed colostrum from other herds?
 - Q20. When was this last fed?
 - Q21. Do you feed milk from cows from other herds
 - Q22. When was this last fed?
 - Q23. Are weaned heifers exposed to cows or their manure at any time?
 - Q24. Are maiden heifers exposed to cows or their manure at any time?
 - Q25. What is the overall hygiene and cleanliness score of weaned heifers
 - Q26. What is the overall hygiene and cleanliness score of maiden or incalf heifers?
 - Q27. Are weaned heifers (≥ 6 months) fed forages that have received slurry from adult animals within the last year?
 - Q28. Are maiden or incalf heifers (≥ 6 months) fed forages that have received slurry from adult animals within the last year?
 - Q29. Dry cow area environment hygiene score
 - Q30. Milking cow area environment hygiene score
 - Q31. Dry cow cleanliness
 - Q32. Milking cow cleanliness
 - Q33. Single or multiple cows in calving areas?
 - Q34. Manure build up
 - Q35. Manure on soiled udders and legs of cows?
 - Q36. Calving area used for lame or sick cows?
 - Q37. Calving area used for JD clinical or JD test positive cows?
 - Q38. Birth of calves in areas other than designated calving area?

			2
Q40. How fast are ne	wborn dairy calves	emoved from their mother	s?

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Table 3. Summary of herd-level characteristics and animal introduction data for 925 dairy herds enrolled in the Irish national Johne's Disease Control Programme. Definition of categories and proportion of herds defined as positive based on ≥ 2 animals testing positive.

Variable	Number in category	Percent in category	Number positive	Percent positive
Herd size			•	t
≤60	246	27%	70	17%
61-80	217	23%	66	23%
81-116	232	25%	61	31%
>116	230	25%	101	44%
Test medium				
Blood	588	64%	166	28%
Milk	337	36%	99	29%
Test precedes RAMP ¹				
Yes	493	53%	157	32%
No	432	47%	108	25%
Herd growth 2005-2014				
<5%	232	25%	56	24%
5-25%	219	24%	66	30%
26-46%	218	24%	67	31%
>45%	256	28%	76	30%
Mean annual purchases 2	$005 - 2009^2$			
Closed/Replacement Bulls Only	101	11%	28	28%
Females at <2% of herd size	266	29%	81	30%
Females at 2-7.5% of herd size	281	30%	72	26%
Females at >7.5% of herd size	277	30%	84	30%
Mean number of herds pu	rchased from 20	005 - 2009		
<0.4	240	26%	70	29%
0.4-1.0	180	19%	51	28%
1.0-2.2	234	25%	71	30%
>2.2	271	29%	73	27%
Beef purchases 2005-2009	3			
Yes	383	41%	107	28%

No	542	59%	158	29%
Moon number of hords nu	urchasod fro	m 2010 2014		
Wean number of nerus pu	ii chaseu ii o	III 2010-2014		
Closed/Replacement Bulls Only	146	16%	43	29%
Females at <2% of herd size	316	34%	87	28%
Females at 2-7.5% of herd size	204	22%	57	28%
Females at >7.5% of herd size	259	28%	78	30%
Beef purchases 2010-2014				
Yes	327	35%	95	29%
No	598	65%	170	28%
Mean number of herds pu	rchased fro	m 2010-2014		
<0.4	363	39%	98	27%
0.4-1.0	209	23%	56	27%
1.0-2.2	195	21%	63	32%
>2.2	158	17%	48	30%

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- 570 1 RAMP = Risk Assessment and Management Plan
- 571 ²Replacement Bulls Only = herds not introducing females and only introducing males at $\leq 5\%$

572 of the overall herd size each year

 3 Beef purchases = herds purchasing males at >5% of the overall herd size each year

574 **Table 4.** Results from multivariable logistic regression model assessing the association 575 between RA questions, animal movement data and the outcome "herd positivity", defined as

576	herds with 2 or more positive animals in the herd
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Variable	n ¹	Coefficient	Odds Ratio	95% Confidence Intervals	р	PAF ²
Herd Size		0.01	1.01	1.01, 1.01	< 0.001	
Test Medium						
Milk	337	0.45	1.57	1.57, 1.57	0.021	9.7%
Blood	588	REF				
Test Month						
January	48	2.12	8.33	3.61, 19.24	< 0.001	5.5%
February	53	1.69	5.42	2.34, 12.57	< 0.001	4.9%
March	69	1.34	3.82	1.77, 8.23	0.001	4.4%
April	114	0.66	1.93	0.96, 3.91	0.064	3.2%
May	160	REF				
June	129	0.38	1.46	0.73, 2.92	0.277	2.0%
July	91	1.53	4.62	2.35, 9.08	< 0.001	8.2%
August	67	1.23	3.42	1.59, 7.38	0.002	4.0%
September	53	1.03	2.8	1.21, 6.5	0.016	2.6%
October	69	1.52	4.57	2.17, 9.64	< 0.001	5.5%
November	44	1.69	5.42	2.33, 12.61	< 0.001	4.2%
December	28	1.19	3.29	1.16, 9.31	0.026	1.5%

Q3. Presence of clinical JD or test positive cows in past³

No and RA conducted after testing	257	REF				
No and RA conducted before testing	348	0.38	1.46	0.91, 2.35	0.114	7.8%
Yes and RA conducted after testing	175	1.03	2.8	1.67, 4.69	< 0.001	12.2%
Yes and RA conducted before testing	145	1.21	3.35	1.92, 5.84	< 0.001	12.6%

Q11. Are calves fed colostrum from own mother or from known low risk colostrum sources?

Calves receive colostrum	291	REF				
from their own test						
negative mother						
Calves receive colostrum	278	0.39	1.48	0.94, 2.31	0.088	6.9%
from their own mother (no						
selection)						
1-10% of calves receive	166	0.35	1.42	0.85, 2.38	0.190	4.2%
colostrum from source						
other than dam						

>10% of calves receive colostrum from source other than dam	190	0.74	2.1	1.28, 3.42	0.003	11.6%
O23. Are weaned heifers ex	posed t	o cows or the	eir manure	at any time?		
Never housed/grazed with adult animals, no direct contact and no exposure to manure. Not fed uneaten rations from cows and not sharing water troughs	241	0.27	1.31	0.85, 2.02	0.212	4.1%
Housed/grazed near cows but no direct or indirect contact	269	0.54	1.72	1.15, 2.55	0.007	10.5%
Housed/grazed near cows, direct or indirect contact possible	415	REF				
Q30. Milking cow environm	nent hy	giene score				
No visible manure contamination of feeding areas or water troughs	188	0.38	1.46	0.95, 2.26	0.084	4.6%
Trace amount of manure visible, feeding areas/water troughs cleaned > 1/week	565	REF				
Manure clearly visible, feeding areas/water troughs cleaned < 1/week	172	0.55	1.73	1.14, 2.63	0.010	7.6%
Q36. Calving area used for	lame or	sick cows?				
Calving area is never used by non-calving cows	516	REF				
Calving area is used by non-calving cows once in 3 months	125	0.05	1.05	0.63, 1.75	0.841	0.5%
Calving area is used by non-calving cows at least once monthly	75	0.28	1.32	0.73, 2.41	0.357	1.7%
Calving area is used by non-calving cows at least once weekly	209	0.81	2.25	1.48, 3.42	<0.001	14.2%
Q40. How quickly are calve	es remov	ved from the	ir dam?			
>90% are removed within 15 minutes of birth	97	REF				
>50% are removed within 30 minutes	507	0.84	2.32	1.23, 4.37	0.010	24.7%
10-50% are removed within 30 minutes	236	0.42	1.52	0.76, 3.03	0.237	5.6%

<10% are removed within	85	0.49	1.63	0.72, 3.7	0.239	3.2%
50 minutes						
Herd Growth						
Stable (<5%)	256	0.23	1.26	0.78, 2.03	0.350	4.2%
Small Growth (5-25%)	219	0.47	1.6	1, 2.56	0.049	6.7%
Medium (26 - 46%)	218	0.41	1.51	0.95, 2.39	0.079	6.1%
Large (>46%)	232	REF				

 1 n = number in category

 2 PAF = Population Attributable Fraction

 ${}^{3}RA = Risk Assessment$

- 581 **Table 5.** Results from final multivariable Bayesian beta regression model assessing the
- association between RA questions, animal movement data and the probability of infection as
- 583 estimated by a Bayesian latent class analysis.

Variable	n ¹	Coefficient	Probability of infection	95% Probability Interval	Proportional reduction in R- squared
Intercept			0.60	0.25, 0.86	
Q3. Presence of clinical J	ID or te	st positive cov	vs in past		
No and after testing	257	REF			
No and before testing	348	0.52	0.72	0.66, 0.77	
Yes and after testing	175	0.08	0.62	0.57, 0.67	
Yes and before testing	145	0.44	0.70	0.65, 0.75	
					22.6%
Test Month					
January	48	0.80	0.77	0.69, 0.83	
February	53	0.66	0.74	0.66, 0.81	
March	69	0.31	0.67	0.59, 0.75	
April	114	0.12	0.63	0.55, 0.69	
May	160	REF			
June	129	0.10	0.62	0.55, 0.69	
July	91	0.49	0.71	0.64, 0.77	
August	67	0.37	0.68	0.60, 0.76	
September	53	0.38	0.69	0.60, 0.76	
October	69	0.63	0.74	0.66, 0.80	
November	44	0.87	0.78	0.70, 0.85	
December	28	0.35	0.68	0.56, 0.78	
					35.3%
Proportion of hard tasta	4				
Increase of 10%	.1	-0.22	0.55		
		0.22	0.00		3.2%
Q28. Are maiden or inca adult animals within the	lf heife last yea	rs (≥6 months ar?) fed forages t	hat have receive	ed slurry from
No forages fed to heifers have been spread with slurry in the previous season	50				
Fresh or conserved forages that were spread with slurry in the	875	0.35	0.68	0.6, 0.76	

1.3%

Q31. Dry cow cleanliness					
No manure visible on	135	0.28	0.67	0.61, 0.72	
hind legs or udder					
Manure present on hind	486	0.00	0.60		
legs but not above					
dewclaws					
Manure present on hind	213	0.14	0.63	0.59, 0.68	
legs but not above hocks,					
or is present on the udder					
or teats					
Manure present above the	91	0.26	0.66	0.60, 0.72	
hocks					
					7.1%

Q36. Is the Calving Area ever used for lame or sick cows?								
Calving area is never	REF							
used by non-calving cows								
Calving area is used by	0.13	0.63	0.57, 0.69					
non-calving cows once in								
3 months								
Calving area is used by	0.14	0.63	0.56, 0.7					
non-calving cows at least								
once monthly								
Calving area is used by non-	0.41	0.69	0.65, 0.74					
calving cows at least once								
weekly								
				5.8%				

584

585 1 n = number in each category

587 McAloon Figure 1. Stacked bar graph showing distribution of responses to Risk Assessment for 925 dairy herds enrolled in the Irish national

- Johne's Disease Control Programme. Questions 23-25 and Question 17 are scored to a maximum 7, questions 26 and 28 are scored to a
- 589 maximum of 4.
- 590

591



592

586

593 McAloon Figure 2. Predicted median probabilities of infection from final Bayesian beta
594 regression model versus data outputs (observed) from Bayesian latent class model. R-squared
595 = 0.16.

